

Figure 1

MKEIAMRNSKRKPEPTPFAGKKLRSTRRLRRKRAQISPVLVQSPPLWSKQIGVSAASVDSCS	60
DLLADDNVSCGSSRVEKSSNPKKTLEEVESKPGYNVKTIGDSKFRRTITRSYKHLHKE	120
KEGDEIEVSESSCVDSNSGAGLRRLNVKGNKINDNEISFSRSDVTFAGHVSNSRSLNFE	180
SENKESDVSVISGVEYCSKFGSVTGADNEEIEISKPSFVEADSSLGSAKELKPELEI	240
VGCVSDLACSEKFSEEVSDSLDDSESSEQRSEIYSQYSDFDYSDYTPSIFFDGSEFSEKS	300
SSDSPISHRSRLYLQFKEQFCRSTIPNDFGSSCEEEIHSELLRFDDEEVEESYLRLRERE	360
RSHAYMRDCAKAYCSRMDNTGLIPRLRSIMVQWIVKQCSDMGLQQETLFLGVGLLDRFLS	420
<u>KGsfKsERTLILVGIASLTLATRIEENQPYNSIRKRNFTIQNLRYSRHEVVAMEWL</u> <u>VQEV</u>	480
<u>LNFKCF</u> <u>TPTIFNFWFLKAAARANPEVERKAKSLAVTSLSDQTQLCFWPSTVAAALVVLA</u>	540
CIEHNKISAYQQRVIKVHVRTTDTNELPECVKSLDWLLGQ	578

Figure 2

424

SDS 377 MDN-TGLIPRLRSIMVQWIVKQCSDMGLQQETFLGVGLLDRFLSKGSF
 cyc2b MAQFDISDKMRAILIDWLVHDKFELMNETLFLTVNLIDRFLSKQAV
 cyc2a M-QQIDLNEKMRAILIDWLVHDKFELMNETLFLTVNLIDRFLSKQNV
 Consensus M + ++R+I++ W++ L +ETLFL+V L+DRFLSK

472

SDS 425 KSERTLILVGIASLTLATRIEE-NQPYNSIRKRNFTIQNLRYSRHEVVA
 cyc2b -ARKKLQVLVGLVALLLACKYEEVSVV---IVEDLVVISDKAYTRTDVLE
 cyc2a -MRKKLQVLVGLVALLLACKYEEVSVV---VVEDLVVISDKAYTRNDVLE
 Consensus + L LVG+ +L LA + EE P + I Y+R +V+

521

SDS 473 MEWLVQEVNFKCFTPTIFNFWFLKAAARANPEVERKAKSLAVTSLSD
 cyc2b MEKIMLSTLQFNMSLPTQYPFLKRFLKAAQSDKKLEILASFLIELALVD
 cyc2a MEKIMLSTLQFNISLPTQYPFLKRFLKAAQADKKCEVLASFLIELALVE
 Consensus ME - L+F PT + FL +LKA A E A L +L D

Figure 3

	SDS	cyc2b	cyc2a	cyc3b	cycD
SDS	100%	34%/52%	34%/52%	28%/49%	21%/42%
cyc2b		100%	87%/92%	40%/60%	21%/43%
cyc2a			100%	46%/64%	22%/43%
cyc3b				100%	22%/41%